



PCT

RAW SEQUENCE LISTING

DATE: 06/22/2005

PATENT APPLICATION: US/10/538,471

TIME: 10:19:58

Input Set : A:\PTO.RJ.txt

Output Set: N:\CRF4\06222005\J538471.raw

3 <110> APPLICANT: Balakireva, Larissa
 5 <120> TITLE OF INVENTION: MOLECULES INHIBITING HEPATITIS C VIRUS PROTEIN SYNTHESIS AND
 METHOD FOR

6 SCREENING SAME
 8 <130> FILE REFERENCE: 1759.200
 C--> 11 <140> CURRENT APPLICATION NUMBER: US/10/538,471
 C--> 11 <141> CURRENT FILING DATE: 2005-06-03
 11 <150> PRIOR APPLICATION NUMBER: PCT/FR03/03675
 12 <151> PRIOR FILING DATE: 2003-12-11
 14 <150> PRIOR APPLICATION NUMBER: FR0215718
 15 <151> PRIOR FILING DATE: 2002-12-12
 17 <160> NUMBER OF SEQ ID NOS: 16
 19 <170> SOFTWARE: PatentIn version 3.1
 21 <210> SEQ ID NO: 1
 22 <211> LENGTH: 326
 23 <212> TYPE: DNA
 24 <213> ORGANISM: Artificial Sequence
 W--> 26 <220> FEATURE: <221> HCV
 27 <222> LOCATION: 40..372

Does Not Comply
 Corrected Diskette Needed

(pg 1, 3-6)
 moved <221> response
 to next line

28 <223> OTHER INFORMATION: corresponds to IRES sequence of HCV
 30 <400> SEQUENCE: 1
 32 ctccccctgtg aagaactact gtcttcacgc agaaagcgtc tagccatggc gttagtatga 60
 34 gtgtcgtgca gcctccagga cccccctcc cgaggagagcc atagtggctc gcggaaccgg 120
 36 tgagtacacc ggaattgcca ggatgaccgg gtcctttctt ggatcaaccc gctcaatgcc 180
 38 tggagatttg ggcgtgcccc cgcgagactg ctagccgagt agtggtgggt cgcgaaaggc 240
 40 cttgtggtac tgctgatag ggtgcttgcg agtgccccgg gaggtctcgt agaccgtgca 300
 42 tcatgagcac aaatcctaaa gaaaaa 326
 45 <210> SEQ ID NO: 2
 46 <211> LENGTH: 80
 47 <212> TYPE: DNA
 48 <213> ORGANISM: Artificial Sequence
 W--> 50 <220> FEATURE: <221> HCV
 51 <222> LOCATION: 40..119
 52 <223> OTHER INFORMATION: corresponds to a portion (region II) of HCV IRES sequence
 54 <400> SEQUENCE: 2
 56 ctccccctgtg aggaactact gtcttcacgc agaaagcgtc tagccatggc gttagtatga 60
 58 gtgttgtgca gcctccagga 80
 61 <210> SEQ ID NO: 3
 62 <211> LENGTH: 37
 63 <212> TYPE: DNA
 64 <213> ORGANISM: Artificial Sequence
 W--> 66 <220> FEATURE: <221> HCV
 67 <222> LOCATION: 56..92
 68 <223> OTHER INFORMATION: corresponds to a portion (consensus sequence) of HCV IRES

same

same

sequence

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70 <400> SEQUENCE: 3
 72 tactgtcttc acgcagaaag cgtctagcca tggcggtt 37
 75 <210> SEQ ID NO: 4
 76 <211> LENGTH: 814
 77 <212> TYPE: PRT
 78 <213> ORGANISM: Artificial Sequence *same*
 W--> 80 <220> FEATURE: <221> p116
 81 <222> LOCATION: 1..814
 82 <223> OTHER INFORMATION: corresponds to p116 subunit of eIF3
 84 <400> SEQUENCE: 4
 86 Met Gln Asp Ala Glu Asn Val Ala Val Pro Glu Ala Ala Glu Glu Arg
 87 1 5 10 15
 90 Ala Glu Pro Gly Gln Gln Gln Pro Ala Ala Glu Pro Pro Pro Ala Glu
 91 20 25 30
 94 Gly Leu Leu Arg Pro Ala Gly Pro Gly Ala Pro Glu Ala Ala Gly Thr
 95 35 40 45
 98 Glu Ala Ser Ser Glu Glu Val Gly Ile Ala Glu Ala Gly Pro Glu Pro
 99 50 55 60
 102 Glu Val Arg Thr Glu Pro Ala Ala Glu Ala Glu Ala Ala Ser Gly Pro
 103 65 70 75 80
 106 Ser Glu Ser Pro Ser Pro Pro Ala Ala Glu Glu Leu Pro Gly Ser His
 107 85 90 95
 110 Ala Glu Pro Pro Val Pro Ala Gln Gly Glu Ala Pro Gly Glu Gln Ala
 111 100 105 110
 114 Arg Asp Glu Arg Ser Asp Ser Arg Ala Gln Ala Val Ser Glu Asp Ala
 115 115 120 125
 118 Gly Gly Asn Glu Gly Arg Ala Ala Glu Ala Glu Pro Arg Ala Leu Glu
 119 130 135 140
 122 Asn Gly Asp Ala Asp Glu Pro Ser Phe Ser Asp Pro Glu Asp Phe Val
 123 145 150 155 160
 126 Asp Asp Val Ser Glu Glu Leu Leu Gly Asp Val Leu Lys Asp Arg
 127 165 170 175
 130 Pro Gln Glu Ala Asp Gly Ile Asp Ser Val Ile Val Val Asp Asn Val
 131 180 185 190
 134 Pro Gln Val Gly Pro Asp Arg Leu Glu Lys Leu Lys Asn Val Ile His
 135 195 200 205
 138 Lys Ile Phe Ser Lys Phe Gly Lys Ile Thr Asn Asp Phe Tyr Pro Glu
 139 210 215 220
 142 Glu Asp Gly Lys Thr Lys Gly Tyr Ile Phe Leu Glu Tyr Ala Ser Pro
 143 225 230 235 240
 146 Ala His Ala Val Asp Ala Val Lys Asn Ala Asp Gly Tyr Lys Leu Asp
 147 245 250 255
 150 Lys Gln His Thr Phe Arg Val Asn Leu Phe Thr Asp Phe Asp Lys Tyr
 151 260 265 270
 154 Met Thr Ile Ser Asp Glu Trp Asp Ile Pro Glu Lys Gln Pro Phe Lys
 155 275 280 285
 158 Asp Leu Gly Asn Leu Arg Tyr Trp Leu Glu Glu Ala Glu Cys Arg Asp
 159 290 295 300
 162 Gln Tyr Ser Val Ile Phe Glu Ser Gly Asp Arg Thr Ser Ile Phe Trp

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```

163 305          310          315          320
166 Asn Asp Val Lys Asp Pro Val Ser Ile Glu Glu Arg Ala Arg Trp Thr
167          325          330          335
170 Glu Thr Tyr Val Arg Trp Ser Pro Lys Gly Thr Tyr Leu Ala Thr Phe
171          340          345          350
174 His Gln Arg Gly Ile Ala Leu Trp Gly Gly Glu Lys Phe Lys Gln Ile
175          355          360          365
178 Gln Arg Phe Ser His Gln Gly Val Gln Leu Ile Asp Phe Ser Pro Cys
179          370          375          380
182 Glu Arg Tyr Leu Val Thr Phe Ser Pro Leu Met Asp Thr Gln Asp Asp
183 385          390          395          400
186 Pro Gln Ala Ile Ile Ile Trp Asp Ile Leu Thr Gly His Lys Lys Arg
187          405          410          415
190 Gly Phe His Cys Glu Ser Ser Ala His Trp Pro Ile Phe Lys Trp Ser
191          420          425          430
194 His Asp Gly Lys Phe Phe Ala Arg Met Thr Leu Asp Thr Leu Ser Ile
195          435          440          445
198 Tyr Glu Thr Pro Ser Met Gly Leu Leu Asp Lys Lys Ser Leu Lys Ile
199          450          455          460
202 Ser Gly Ile Lys Asp Phe Ser Trp Ser Pro Gly Gly Asn Ile Ile Ala
203 465          470          475          480
206 Phe Trp Val Pro Glu Asp Lys Asp Ile Pro Ala Arg Val Thr Leu Met
207          485          490          495
210 Gln Leu Pro Thr Arg Gln Glu Ile Arg Val Arg Asn Leu Phe Asn Val
211          500          505          510
214 Val Asp Cys Lys Leu His Trp Gln Lys Asn Gly Asp Tyr Leu Cys Val
215          515          520          525
218 Lys Val Asp Arg Thr Pro Lys Gly Thr Gln Gly Val Val Thr Asn Phe
219          530          535          540
222 Glu Ile Phe Arg Met Arg Glu Lys Gln Val Pro Val Asp Val Val Glu
223 545          550          555          560
226 Met Lys Glu Thr Ile Ala Phe Ala Trp Glu Pro Asn Gly Ser Lys
227          565          570          575
230 Phe Ala Val Leu His Gly Glu Ala Pro Arg Ile Ser Val Ser Phe Tyr
231          580          585          590
234 His Val Lys Asn Asn Gly Lys Ile Glu Leu Ile Lys Met Phe Asp Lys
235          595          600          605
238 Gln Gln Ala Asn Thr Ile Phe Trp Ser Pro Gln Gly Gln Phe Val Val
239          610          615          620
242 Leu Ala Gly Leu Arg Ser Met Asn Gly Ala Leu Ala Phe Val Asp Thr
243 625          630          635          640
246 Ser Asp Cys Thr Val Met Asn Ile Ala Glu His Tyr Met Ala Ser Asp
247          645          650          655
250 Val Glu Trp Asp Pro Thr Gly Arg Tyr Val Val Thr Ser Val Ser Trp
251          660          665          670
254 Trp Ser His Lys Val Asp Asn Ala Tyr Trp Leu Trp Thr Phe Gln Gly
255          675          680          685
258 Arg Leu Leu Gln Lys Asn Asn Lys Asp Arg Phe Cys Gln Leu Leu Trp
259          690          695          700

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262 Arg Pro Arg Pro Pro Thr Leu Leu Ser Gln Glu Gln Ile Lys Gln Ile
 263 705 710 715 720
 266 Lys Lys Asp Leu Lys Lys Tyr Ser Lys Ile Phe Glu Gln Lys Asp Arg
 267 725 730 735
 270 Leu Ser Gln Ser Lys Ala Ser Lys Glu Leu Val Glu Arg Arg Arg Thr
 271 740 745 750
 274 Met Met Glu Asp Phe Arg Lys Tyr Arg Lys Met Ala Gln Glu Leu Tyr
 275 755 760 765
 278 Met Glu Gln Lys Asn Glu Arg Leu Glu Leu Arg Gly Gly Val Asp Thr
 279 770 775 780
 282 Asp Glu Leu Asp Ser Asn Val Asp Asp Trp Glu Glu Glu Thr Ile Glu
 283 785 790 795 800
 286 Phe Phe Val Thr Glu Ile Ile Pro Leu Gly Asn Gln Glu
 287 805 810

290 <210> SEQ ID NO: 5

291 <211> LENGTH: 106

292 <212> TYPE: PRT

293 <213> ORGANISM: Artificial Sequence

W--> 295 <220> FEATURE: <221> p116

296 <222> LOCATION: 175..279

297 <223> OTHER INFORMATION: corresponds to a portion (RRM) of eIF3 p116 subunit

299 <400> SEQUENCE: 5

301 Met Asp Arg Pro Gln Glu Ala Asp Gly Ile Asp Ser Val Ile Val Val
 302 1 5 10 15

305 Asp Asn Val Pro Gln Val Gly Pro Asp Arg Leu Glu Lys Leu Lys Asn
 306 20 25 30

309 Val Ile His Lys Ile Phe Ser Lys Phe Gly Lys Ile Thr Asn Asp Phe
 310 35 40 45

313 Tyr Pro Glu Glu Asp Gly Lys Thr Lys Gly Tyr Ile Phe Leu Glu Tyr
 314 50 55 60

317 Ala Ser Pro Ala His Ala Val Asp Ala Val Lys Asn Ala Asp Gly Tyr
 318 65 70 75 80

321 Lys Leu Asp Lys Gln His Thr Phe Arg Val Asn Leu Phe Thr Asp Phe
 322 85 90 95

325 Asp Lys Tyr Met Thr Ile Ser Asp Glu Trp
 326 100 105

329 <210> SEQ ID NO: 6

330 <211> LENGTH: 33

331 <212> TYPE: DNA

332 <213> ORGANISM: Artificial Sequence

W--> 334 <220> FEATURE: <221> primer_bind

335 <222> LOCATION: 1..33

336 <223> OTHER INFORMATION: HCV RRM 5' primer (RRMfwd)

338 <400> SEQUENCE: 6

340 catatggatc ggccccagga agcagatgga atc

33

343 <210> SEQ ID NO: 7

344 <211> LENGTH: 33

345 <212> TYPE: DNA

346 <213> ORGANISM: Artificial Sequence

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Input Set : A:\PTO.RJ.txt

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W--> 348 <220> FEATURE: <221> primer_bind ← Same
 349 <222> LOCATION: 1..33
 350 <223> OTHER INFORMATION: HCV RRM 3' primer (RRMrev)
 352 <400> SEQUENCE: 7
 354 gtgctcgagc cactcgtcac tgatcgatcat ata 33
 357 <210> SEQ ID NO: 8
 358 <211> LENGTH: 29
 359 <212> TYPE: DNA
 360 <213> ORGANISM: Artificial Sequence

W--> 362 <220> FEATURE: <221> primer_bind ← Same
 363 <222> LOCATION: 1..29
 364 <223> OTHER INFORMATION: HCV IRES 5' primer (IRESfwd)
 366 <400> SEQUENCE: 8
 368 accgctagcc tcccctgtga ggaactact 29
 371 <210> SEQ ID NO: 9
 372 <211> LENGTH: 46
 373 <212> TYPE: DNA
 374 <213> ORGANISM: Artificial Sequence

W--> 376 <220> FEATURE: <221> primer_bind ← Same
 377 <222> LOCATION: 1..46
 378 <223> OTHER INFORMATION: HCV IRES 3' primer (IRESrev)
 380 <400> SEQUENCE: 9
 382 gaaagctttt ttctttgagg tttaggattt gtgctcatga tgcacg 46
 385 <210> SEQ ID NO: 10
 386 <211> LENGTH: 95
 387 <212> TYPE: DNA
 388 <213> ORGANISM: Artificial Sequence

W--> 390 <220> FEATURE: <221> primer_bind ← Same
 391 <222> LOCATION: 1..95
 392 <223> OTHER INFORMATION: primer IIIabcfwd which corresponds to T7 polymerase promoter
 + 139-215 of
 393 HCV (regions IIIa-IIIb)
 395 <400> SEQUENCE: 10
 397 taatacgact cactataggg tagtggtctg cggaaccggt gactacaccg gaattgccag 60
 399 gacgaccggg tcctttcttg gataaaccg ctcaa 95
 402 <210> SEQ ID NO: 11
 403 <211> LENGTH: 60
 404 <212> TYPE: DNA
 405 <213> ORGANISM: Artificial Sequence

W--> 407 <220> FEATURE: <221> primer_bind ← Same
 408 <222> LOCATION: 1..60
 409 <223> OTHER INFORMATION: primer IIIabcrev which corresponds to 193-252 of HCV
 (regions IIIb-IIIc)
 413 <400> SEQUENCE: 11
 415 tagcagtctc gcgggggcac gcccaaattc ccaggcattg agcgggttga tccaagaaag 60
 418 <210> SEQ ID NO: 12
 419 <211> LENGTH: 20
 420 <212> TYPE: DNA
 421 <213> ORGANISM: Artificial Sequence

W--> 423 <220> FEATURE: <221> primer_bind ← Same
 424 <222> LOCATION: 1..20

RAW SEQUENCE LISTING ERROR SUMMARY

DATE: 06/22/2005

PATENT APPLICATION: US/10/538,471

TIME: 10:19:59

Input Set : A:\PTO.RJ.txt

Output Set: N:\CRF4\06222005\J538471.raw

Invalid Line Length:

The rules require that a line not exceed 72 characters in length. This includes spaces.

Seq#:10; Line(s) 392

L-72.

VERIFICATION SUMMARY

DATE: 06/22/2005

PATENT APPLICATION: US/10/538,471

TIME: 10:19:59

Input Set : A:\PTO.RJ.txt

Output Set: N:\CRF4\06222005\J538471.raw

L:11 M:270 C: Current Application Number differs, Replaced Current Application No
L:11 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:26 M:256 W: Invalid Numeric Header Field, <220> has non-blank data
L:50 M:256 W: Invalid Numeric Header Field, <220> has non-blank data
L:66 M:256 W: Invalid Numeric Header Field, <220> has non-blank data
L:80 M:256 W: Invalid Numeric Header Field, <220> has non-blank data
L:295 M:256 W: Invalid Numeric Header Field, <220> has non-blank data
L:334 M:256 W: Invalid Numeric Header Field, <220> has non-blank data
L:348 M:256 W: Invalid Numeric Header Field, <220> has non-blank data
L:362 M:256 W: Invalid Numeric Header Field, <220> has non-blank data
L:376 M:256 W: Invalid Numeric Header Field, <220> has non-blank data
L:390 M:256 W: Invalid Numeric Header Field, <220> has non-blank data
L:407 M:256 W: Invalid Numeric Header Field, <220> has non-blank data
L:423 M:256 W: Invalid Numeric Header Field, <220> has non-blank data
L:437 M:256 W: Invalid Numeric Header Field, <220> has non-blank data
L:453 M:256 W: Invalid Numeric Header Field, <220> has non-blank data
L:467 M:256 W: Invalid Numeric Header Field, <220> has non-blank data
L:481 M:256 W: Invalid Numeric Header Field, <220> has non-blank data